



FIG. 1

Table 1

Table 2

Table 3

Table 4

Table 5

***Streptococcus mutans* UAB159 (119 aa)**

Amino acid sequence:

VLKKAYRVKSDKDFQAI FTEGRSVANRKFVVYSLEKDQSHYRVGLSVGKRLGNVVRNAIKRKL RHVLMELGPYLGT  
QDFVVIARKGVEELDYSTMKKNLVHVLKLAKLYQEGSIREKE

Nucleotide sequence (plus strand):

AGATTTTGGCTTTTCTCATTTTATGATATAATAGTGATAATTTAAATATTGGAGTCATGTTTGAAAAAGCCTA  
TCGCGTTAAAAGTGATAAAGATTTTCAGGCAATTTTACTGAAGGACGAAGTGTTGCCAATCGGAAATTTGTTGTCT  
ATAGTTTAGAAAAAGATCAAAGTCACTATCGTGTTGGACTTTTCAGTTGGAAAAAGATTAGGAAATGCTGTCGTTAGA  
AATGCGATTAAACGAAAATTGCGCCATGTCCTTATGGAACCTGGTCCTTATTTAGGCACTCAAGATTTTGTGTTAT  
TGCTAGAAAAGGTGTTGAGGAACCTGATTATAGCAGCATGAAAAAAATCTGGTTCATGTTTTAAACTGGCTAAAC  
TGTATCAGGAAGGATCTATTCGTGAAAAAGAA

Sequence origin: University of Oklahoma ACGT; Contig 299

**FIG. 2A**

***Klebsiella pneumoniae* M6H 78578 (119 aa)**

Amino acid sequence:

VVKLAFFPRELRLLTTPSHFTFVFQOPQORAGTPQITILGRNLNLGHPRIGLTVAKKNVKRAHERNRIKRLTRESFRLRQ  
HELPPMDFV VVAKRGVADLDNRALSEALEKLWRRHCRLARGS

Nucleotide sequence (plus strand):

CGTCGTCGTGCTAAAGGCCGCGCTCGTCTGACCGTTTCCAAGTAATAAAGCTAACCCTGCGTGGTTAAGCTCGCATT  
TCCCAGGGAGTTACGCTTGTAACTCCAGTCATTTCACTTTTCGTCTTCCAGCAGCCACAACGGGCTGGCAGCGCCG  
AAATCACCATCCTCGGCCGCTGAATTCGCTGGGGCATCCCCGCATCGGTCTCACCCTCGCCAAGAAAAACGTGAAA  
CGCGCACATGAACGCAATCGGATTAAACGTCTGACGCGTGAAAGTTTTCGTTTGGGTCAACATGAACCCCCGCAAT  
GGATTTTCGTGGTGGTGGCGAAAAGAGGGGTGCGGACCTCGATAACCGTGCTCTCTCGGAAGCGTTGGAAAAATTAT  
GGCGCCGCCATTGTCGCTGGCTCGCGGGTCCGATCGGCTGATTTCAGAGTTTATCAGCGCCTGATTAGTCCGCTAC  
TCGGGCCCGCATTGTC

Sequence origin: Washington University; Contig 632

**FIG. 2B**

***Salmonella paratyphi* A ATCC 9150 (110 aa)**

Amino acid sequence:

VTFVNSRSFHIRLPATSTGCTPQITILGRNLNLGHPRIGLTVAKKNVRRRAHERNRIKRLTRESFRLRQHHELPAMDVF  
VVAKKGVADLDNRALSEALEKLWRRHCRLARGS

Nucleotide sequence (plus strand):

CTGACCGTTTCCAAGTAATAAAGCTAACCCTGAGTGGTTAAGCTCGCATTTCAGGGAGTTACGTTTGTAACTC  
CCGCTCATTTACATTCGTCTTCCAGCAACCTCAACGGGCTGCACGCCGCAAATCACCATCCTCGGCCGCTGAATT  
CGCTGGGGCATCCCCGATCGGTCTTACCGTCGCCAAGAAAAATGTTTCGACGTGCGCATGAACGCAACCGGATTAAA  
CGTCTGACGCGTGAAAGCTTCCGTCTGCGCCAGCATGAACTTCCTGCAATGGATTTTCGTGGTGGTGGCGAAAAAAGG  
GGTTGCCGACCTCGATAACCGTGCTCTCTCGGAAGCGTTGGAAAAATTATGGCGCCGCCACTGTCGCTGGCTCGCG  
GGTCCTGATAGCCCTTATTCGGGTCTATCAACGCCTGATCAGTCCGCTGCTTGGGCCGATTGTCGTTTC

Sequence origin: Washington University;

**FIG. 2C**

*Pseudomonas aeruginosa* PAO1 (135 aa)

Amino acid sequence:

VVSRDFDRDKRLLTARQFSVFDSPGKVPKGVHLLARENGLDHPRLGLVIGKKNVKLAVQRNRLKRLIRESFRHN  
QETLAGWDIVVIARKGLGELENPELHQQFGKLWKRLLRNRPRTESPADAPGVADGTHA

Nucleotide sequence (plus strand):

TCTGTGCGGTCGTCGCGCCAAAGGCCGTAAGCGTCTGACCGTCTGATTTATCCGGTACGGGTCGTGAGTCGGGACTT  
CGACCGGGACAAGCGTCTACTGACAGCCCGGCAATTCAGCGCAGTCTTCGACTCTCCGACCGGCAAGGTCCCCGGCA  
AGCACGTCTGTGCTGGCGCGGAGAACGGTCTCGATCACCCCGCCTGGGCCTGGTGATCGGCAAGAAGAACGTC  
AAGCTCGCCGTCCAGCGCAATCGCCTCAAACGCCTGATCCGCGAATCGTTCGCCATAACCAGGAAACCCTGGCTGG  
CTGGGATATCGTGGTGATCGCGCGCAAAGGCCGGAAGTGGAAATCCGGAGCTGCACCAGCAGTTCGGCAAGC  
TCTGGAAACGCCTGTTGCGCAATCGACCTCGCACGGAAAGCCCTGCTGACGCCCCCTGGCGTGCGCGACGGTACTCAT  
GCATAGGTGCGATGCCCCGCGCATCCCATCCCTGTAGTGTATCCCCCTTCGATGACCCGGCACCG

Sequence origin: Pathogenesis & University of Washington; Contig 54

## FIG. 2D

*Corynebacterium diphtheriae* (129 aa)

Amino acid sequence:

VTLTSSNRRTTVLPSQHKLSNSEQFRATIRKGRAGRSTVVLHFYAEATAGNLATAGGPRFGLVVSKAVGNAVTRHRV  
SRQLRHVVIAMKDQFPASSHVVRIPPAATASYEELRADVQAALDKLNRKR

Nucleotide sequence (plus strand):

CCGGTCGCGCAATCGTGGCTGCACGTCGTAACAAGGGTCGTAAGAGCCTGACCGCTTAAGGTCACTCTTACAAGCTC  
GAATAGAACGACGGTGCTACCTTCACAGCACAAGCTCAGCAATTCCGAACAGTTCCGCGCAACGATTCCGGAAGGGCA  
AGCGTGCTGGGAGGAGCACCGTCGTTCTTCAATTTTATGCTGAGGCGACCGCGGGCAACCTTGCAACCGCAGGCGGC  
CCGCGATTCCGGCTCGTTGTGTCCAAGGCTGTTGGAAATGCTGTGACTCGTCACCGTGTTTCGCGGCAGTTAAGGCA  
CGTAGTAATCGCTATGAAAGACCAGTTCACAGCGTCATCCCATGTTGTTGTGAGGGCGATACCGCCAGCGGCGACAG  
CAAGTTATGAGGAGTTGCGGGCAGATGTGCAGGCAGCACTCGACAAGCTCAACCGCAAGCGATTAAGGCGGTTACTCG  
CCCTCGTGGGCTGGTTAGTCGCGCATTGTTTGTATGCGGTGCGGTTCTA

Sequence origin: Sanger centre; Contig 390

## FIG. 2E

*Chlamydia trachomatis* MoPn (119 aa)

Amino acid sequence:

VHRLTLPKSARLLKRKQFVYVQRGQYCRDQATLRIVPSRHSNIRKGVTVSKKFGKAHQNRNFRKRVREAFRHVR  
PNLPACQVVVSPKGGTLPNFGKLSADLLKHIPEALPLVTSSK

Nucleotide sequence (plus strand):

GCTACAAAAAGTGGAAGAAATCTTTTAAATCGTCGTCGCCGTACGGCAGACATTCCTTAATTGATCTCTAAGATCT  
TTCATTTGTCCATCGGTTAACTCTACCTAAAAGTGCCCGCCTATTGAAACGTAAACAATTTGTTTACGTGCAGCGTT  
GTGGCAATATTGTCGTACTGATCAGGCAACTTTACGAATAGTTCCTTCTCGTCATTTCGAACATCCGTAAAGTAGGG  
GTTACTGTTTCTAAAAAATTTGGGAAAGCCCATCAGCGCAATCGCTTTAAAGAATTGTGCGAGAGGCTTTTAGGCA  
TGTGCGACCAATCTTCCCGCATGTCAAGTGGTAGTGTCTCTAAAGGGGGCACTCTACCAAATTTTGGTAAACTAT  
CCGCGGATCTTCTTAAGCATATTCCAGAGGCTTTGCCTCTCGTTACTTCTTCTAAGTAGTTTTTTTATTTTGGTCAAA  
AAATAAAAAACCATTCCACGCTATAGAGGCATGGAATGGGAA  
Sequence origin: TIGR & Manitoba University;

## FIG. 2F

***Streptococcus pyogenes* M1 (113 aa)**

Amino acid sequence:

VKREKDFQAI FKDGKSTANRKFVIYHLNRGQDHFVRVIGSVGKKIGNAVTRNAVKKIRHVIMALGHQLKSEDFVVIA  
RKGVESLEYQELQQNLHHVHLKLAQLLEKGFEESEKH

Nucleotide sequence (minus strand):

GTTACCTCACCACGACCACAGGCCACTAATAATAGAACTAAGGGGACTATTCTTGCAATTTTAATGTTTTTCTTCAC  
TCTCAAAACCTTTCTCAAGCAATTGTGCTAACTTTAAAACATGATGTAAATTTTGTTGAAGCTCTTGATACTCCAAA  
GATTCGACACCCCTTACGGGCAATCACCACGAAATCCTCTGACTTCAGCTGATGCCCTAATGCCATGATAACATGACG  
TATCTTTTCGTTTGACTGCATTTCTGGTGACTGCATTTCTATTTTTTACCGACAGAAATACCCACACGGAAGTGGT  
CTTGGCCTCTATTTAAATGATAAATGACAAATTTTCGATTTGCTGTACTTTTTCCATCCTTAAATATGGCTTGAAA  
TCTTTCTCACGCTTGACACGATAGGTCTTCTTCAAAATTTAACTCCAATATCTAAATTATTACCATTATACCACATC

Sequence origin: University of Oklahoma ACGT; Contig 7

**FIG. 2J**

***Bordetella pertussis* Tohama I (123 aa)**

Amino acid sequence:

MPRATLPAEARLHRPSEFAAALKGRRLARGAFFIVSASPCAPADDQPARARLGLVIAKRFAARAVTRNTLKRVI  
FRARRLALPAQDYVVRLLHSLTPASLTALKRSARAEVDAHFTRIAR

Nucleotide sequence (minus strand):

CCACCCAGGGGCTGAGGAAGTACCGGTAAACCGGATCGGGGCGATAAGCAGTCTCCTGATCATCGCGCTATCCGCTG  
TGAAGTGAGCATCTACTTCGGCGCGCGCCGAGCGTTTCAGGGCCGTGAGGCTTGCCGGTGTGAGCTTGCTGTGAGC  
CGCACCACGTAATCCTGGGCGCGGAGGCAAGCCGCGGAGCCGGAACGCTTCGCGGATGACCCGCTTCAAGGTATT  
GCGCGTCACGGCGCGGGCGGCAAAACGCTTGGCGATCACCAGGCCAGGCGCGCGCGCGCGCGCGGCTGGTCATCAGCAG  
GGGCACAGGGCGAGGCGCTGACAATAAAGAAAGCCCTCGGGCCAGTCGCCGGCCTTTGAGGGCGGCGGCAAACTCG  
GAGGGGCGATGCAATCGCGCTCCGAGGGAGCGTGGCGCGCGGCGATGGGTGACGTGACGGAGACTGGCGACGGGGC  
CGGCGGCGATGCTCCTGTTACAGGCAATCC

Sequence origin: Sanger centre & MDS; Contig 267

**FIG. 2K**

***Porphyromonas gingivalis* W83 (137 aa)**

Amino acid sequence:

MTSPPTFGLSKSERLYLRDEINTVFGEKAFVVYPLRVVYRLGSEHRVAYSSMLVSVAKKRFRRAVKRNRVKRLVRE  
AYRLNKHLLNDVLQERQIYATIAFMVVSDELDPDFTVERAMQKSLIRIAGNVPSSALKNE

Nucleotide sequence (minus strand):

AGAAGAAAATGGGGAGCAGTAAGAGTTGCACGAGAAAAGCCTTGATCAGTCGCATCGTATTACTCGTTTTTCAAAG  
CCGATGAAGGTACATTTCCGGCAATTCTGATCAGACTCTTTTGCATCGCTCTCTCCACTGTACGAAAGTCAGGAAGT  
TCATCCGATACTACCATAAATGCAATAGTAGCATAGATCTGTCTCTCTTGGAGGACATCGTTTCAAGAGGTGTTTGT  
GAGCCGATAAGCCTCCCTGACCAAACGCTTGACCCTATTGCGCTTTCACGGCTCGCCTAAACCTTTTCTTGCTACGC  
TTACCAGCATGGAGGAATATGCAACTCGATGCTCCGATCCCAGACGGTAGACTACGCGTAGAGGATAAACGACAAAC  
GCCTTGCTTTCGCCAAAGACCGTATTGATTTTCATCGCGAAGATAGAGGCGTTTCGCTTTTGGATAGGCCGAATGTAGG  
CGGAGAGGTCAATTCCTCCGTTGAGGTAATCCTCTAATGCCATAGCCATAGAAGGATATTGCTCGGTGCGCGCA

Sequence origin: TIGR & Forsyth Dental Center

**FIG. 2L**

***Streptococcus pneumoniae* Type 4 (124 aa)**

Amino acid sequence:

VLKKNFRVKREKDFKAI FKEGTSFANRKFVVYQLENQKNRFRVGLSVSKKLGNVTRNQIKRRIRHIIQNAKGS LVE  
DVDFVVIARKGVETLGYAEMEKNLLHVLKLSKIYREGNGSEKETKVD

Nucleotide sequence (minus strand):

TCGCTAGTTACCCCATTTAGTCGCACAGGCTGTCATGATTAAACAGAGACAGTCCTAGCAAACTAGTCAACTTTAGTTT  
CTTTTTCACTCCCATTTCCTTCCCGGTAAATCTTTGATAATTTTAATACATGGAGTAGATTTTCTCCATCTCTGCG  
TATCCCAAGGTTTCGACTCCTTTTCGAGCAATGACAACAAAGTCGACATCTTCTACCAGACTCCCTTTTGCAATTCTG  
GATAATATGCCGAATCCGTCGCTTAATTTGATTCTAGTGACGGCATTCCCCAGTTTTTTTGCTAACTGATAGACCTA  
CTCGAAAACGGTTTTTCTGGTTTTCTAATTGGTAGACCACAAATTTGCGATTAGCAAAACTGTCCCCTCCTTGAAA  
ATCGCCTTAAATCTTCTCTCTTTTACACGAAAGTTTTCTTCAAAACTCAACTCCATCTATTAAATTACTACTA  
TTATACCATATTTTTCAAAAAGCCAATCATAG

Sequence origin: TIGR;

**FIG. 2M**

***Clostridium difficile* 630 (epidemic type X) (114 aa)**

Amino acid sequence:

MDFNRTKGLKKDSDFRKVYKHGKSFANKYLVIIYILKNKSDYSRVGISVSKKVGKAITRNRVRRLIKEAYRLNIDEKI  
KPGYDIVFIARVSSKDATFKDIDKSIKNLVKRTDISI

Nucleotide sequence (minus strand):

TCCTTTAATATATAAATTATTTTATTCAAAGTCATTAACCTCCATATTTATAGCATACAATTAATAGAAATATCCG  
TTCTTTTAACTAAATTTTATAGACTTGCTCTATGCTTTTAAAGTAGCATCCTTACTAGATACCCTTGCTATAAAT  
ACTATATCATATCCAGGCTTAATTTTTCATCAATATTTAATCTGTAGGCTTCTTTTATTAATCTTCTTACTCTATT  
CCTAGTAATAGCTTTTCTTACTTTTTTTGAAACAGAAATACCTACTCTACTATAATCTGATTTATTTTAAAGTATAT  
ATATTACTAAATATTTGTTTGCAAAAGATTGGCCGTGTTTATATACTTTTCTAAATCAGAGTCTTTTTTCAACCCT  
TTAGTCCTATTAAAGTCCATAGTTAACCTCCATAAACACAGCTATGAATCGTAATTATTTACACAAAAGGCCACCT  
TTG

Sequence origin: Sanger centre; Contig 975

**FIG. 2N**

***Camphylobacter jejuni* NCTC (108 aa)**

Amino acid sequence:

VKNFDKFSTNEEFSSVYKVGKKWHCEGVII FYLNSYEKKI AVVASKKVGKAVVRNRSKRILRALFAKFERYLQDGKY  
IFVAKNEITELSF SRLEKNLKWGLKKLECFK

Nucleotide sequence (minus strand):

AAGCAGCGGGTTTTAAAGGGCTTAAGAATTTCTGATAAAAAACGGAGTATTTT TAGGCATATCATTTGAAACATTCTA  
GTTTTTCAATCCCCATTTTAGATTTTTTCTAACCTAGAAAAAGAAAGTTCAGTGATTTTCATTTT TAGCTACAAAA  
ATATATTTGCCATCTTGAAGATATCTTTCAAACCTAGCAAACAAAGCTCTTAAAAATTCGTTTTGAACGATTTCTAAC  
CACTGCTTTTCCAACTTTTTACTAGCAACAACCTGCTATTTTTTTTTCATAACTATTCAGATAAAAAATGATCACAC  
CTTCGCAATGCCATTTTTTGCTTACTTTATATACAGATGAAAATTCCTCGTTTGTGCTAAATTTATCAAATTTTTTC  
ACACAGCAAGTCTTTTTCTACCTTTAGCGCGTCTTGCAATTGATCACTTTGCGACCATTTTTTA

Sequence origin: Sanger centre & MDS

**FIG. 2O**

*Vibrio cholerae* serotype O1, Biotype El Tor, Strain N16961 (122 aa)

Amino acid sequence:

SRIILSTYAFNRELRLLTPEHYQKVFFQQAHSAGSPHLTIIARANNLSHPRLGLAVPKKQIKTAVGRNRFKRICRESF  
RLHQNLANKDFVVIKSAQDLSNEELFNLLGKLWQRLSRPSRG

Nucleotide sequence (minus strand): \*NO INITIATOR CODON BEFORE STOP\*

GGCAGCGTGGGCCGATAAGTGGACTAATAAACCACTGGTAAAGTTTTACAATACCAATGGCTAACCACGAGAAGGGC  
GAGAGAGGCGTTGCCATAGTTTGCCAAGCAAGTTAAACAGTTCTTCATTGCTCAAATCTTGCGCGCTCTTTTGGCG  
ATGACAACAAAATCTTTGTTAGCCAGTTGATTTTGATGTAAGCGAAAGCTTCTCTGCAAATACGTTTGAATCGATT  
ACGGCCGACGGCAGTTTTGATCTGCTTTTTAGGAACCGCGAGTCCCAAACGAGGATGAGAAAGGTTATTAGCGCGAG  
CGATGATTGTGAGATGAGGAGAACCAGCACTGTGAGCTTGCTGGAAGACTTTTTGATAATGTTGCGGAGTTAACAAA  
CGTAACTCCCGATTGAATGCGTACGTACTCAAATAATTCGAGATTATTTTGACAGGCGCTTACGGCCTTTTGACAG  
ACGTGCATTTCAGAACTTTACGACCGTTTCG

Sequence origin: TIGR

## FIG. 2G

*Neisseria gonorrhoea* FA 1090 (123 aa)

Amino acid sequence:

VILDYRFRQYRLLKTDDFSSVFAFRNRRSRDLLQVSRNNGLDHPRIGLVVGKKTAKRANERNYMKRVIRDWFRL  
NKNRLPPQDFVVRVRKFDRAKQARAELAQLMFGNPATGCGKQV

Nucleotide sequence (minus strand):

ATGTTCTTGTATGGGAAACCGTTGCCGTCTGAACCTTGCTGCAGGGTACCGTTCTGATCATACCTGTTCCCGC  
ATCCGGTTGCGGGGTTGCCGAACATGAGTTGTGCCAGTTCCGCCCTTGCTGTTTTGCGGTAGCCCTGTGCAATTT  
CGGCGGACGCGCAGCAGAAATCCTGAGGCGGCAGCCGTTTTTTGTTCAATCTGAACCACTGCGGATGACGCGTTT  
CATATAGTTCCGCTCGTTGGCGCGTTTGGCGGTTTTTTTGCCGACCACCAGACCGATGCGGGGATGTTCCAGCCCGT  
TGCCGTTTGAGCGCGAACTTGACAGAGTTCGCGGCTGCGGCGGTTTCTGAATGCAAAAACCGATGAAAAATCATCC  
GTTTTTAACAAGCGGTACTGCCTTCCGAAGCGGTAGTCCAAAATTACACTGCCAGGCGTTTGGCGCCTTTGGCACGG  
CGTGCGGCCAATACTGCGCGTCCGCCGCGT

Sequence origin: University of Oklahoma ACGT; Contig 60

## FIG. 2H

*Neisseria meningitidis* serogroup A Strain Z2491 (123 aa)

Amino acid sequence:

VILDYRFRQYRLLKTDDFSSVFAFRNRRSRDLLQVSRNNGLDHPRIGLVVGKKTAKRANERNYMKRVIRDWFRL  
NKNRLPPQDFVVRVRKFDRAKQARAELAQLMFGNPATGCRKQA

Nucleotide sequence (minus strand):

TGTTCTTAGTATGGGAAACCGTTGCCGTCTGAACCTTGCTGCAGAGTACCGTTCTGATCATGCCTGTTTCCTGC  
ATCCGGTTGCGGGGTTGCCGAACATGAGTTGTGCCAGTTCCGCCCTTGCTGTTTTGCGGTAGCCCTGTGCAATTTA  
CGGCGGACGCGCAGCAGAAATCCTGCGGCGGCAGCCGTTTTTTGTTCAATCTGAACCACTGCGGGATGACGCGCTT  
CATATAATTTCTGTTGTTGGCGCGTTTGGCGGTTTTTTTGCCGACCACCAGACCGATGCGGGGATGATCCAGCCCGT  
TGCCGTTTGAAACGCGAACTTGACAGAGTTCGCGGCTGCGGCGGTTTCTGAATGCAAAAACCGATGAAAAATCATCC  
GTTTTCAACAAGCGGTACTGCCTTCCGAAGCGGTAGTCCAAAATTACACCGCCAGGCGTTTGGCGCCTTTGGCGCGC  
CGTGCGGCCAATACTGCGCGTCCGCCGCGC

Sequence origin: Sanger centre & Oxford University

## FIG. 2I

***Bacillus anthracis* Ames (119 aa)**

Amino acid sequence:

MKKKHRIKKNDEFQTVFQKGKSNANRQFVVYQLDKEEQPNFRIGLSVSKKIGNAVVRNRIKRMIRQSITELKDEIDS  
GKDFVIIARKPCAEMTYEELKKS LIHVFKRSGMKRIKSSVRK

Nucleotide sequence (minus strand):

TAAACCTAATTTCTTTTCAAAGCCTACTCCTCCTTGATCGGTATGTATATAGTGTAATTCATTTCTTACGCTAC  
TTTTTATTCTTTTCATACCAGAGCGTTTAAAGACATGAATTAAGCTTTTCTTTAATTCTTCATATGTCATCTCTGCA  
CAAGGCTTCCTTGCTATTATAACAAAATCTTTCCAGAATCTATCTCATCTTTTAATTCTGTGATCGACTGGCGAAT  
CATACGTTTAATTCGGTTACGCACTACTGCATTTCTTATCTTCTTGCTGACAGAAAGGCCAATACGAAAGTTTGGCT  
GCTCTTCTTTATCTAGTTGATAGACAACAAATTGACGATTTCGCATTCGATTTTCCTTTTGA AAAAACCGTCTGGAAT  
TCATCATCTTTTATACGATGTTTTTCTTCATATCAATTGACACTCCTGTAGTTCATCAGCGGAAATTCACTAT  
TATTAGAAAAAAGACCA

Sequence origin: TIGR;

**FIG. 2P**

***Mycobacterium avium* 104 (119 aa)**

Amino acid sequence:

VLPARNRMTRSTEFDATVKHGTRMAQPDIVVHLRRDSEPDDESAGPRVGLVVGKAVGTAVQRHRVARRLRHVARALL  
GELEPSDRLVIRALPGSRTASSARLAQELQRCLRRMPAGTGP

Nucleotide sequence (minus strand):

GTCCGCGGGCGACGGTTTCGGCCGGCGCCGCGAATGGCCGCGCCCGACCGCGCCGGTCCGGTTCACGGCCCCGGTTCCCG  
CCGGCATGCGCCGCAGGCACCGCTGCAGTTCTTGCGCCAGGCGCGCCGACGACGCGGTCCGGCTTCCGGGCAGCGCG  
CGAATCACCAGCCGGTCGGATGGTTTCGAGTTTCGCCGAGCAGGGCCCCGGGCCACGTGACGCAGCCGGCGGGCCACGCG  
GTGTCGTTGCACCGCCGTCCCGACGGCCTTCCCGACGACCAGCCCCGACCGTGGGCCCCGGGATTTCGTCGTCGGGTT  
CGGAGTCGCGCCGGAGGTGGACGACGATGTCGGGCTGCGCCATGCGGGTTCGCTTCACCGTCGCGTCAAACTCG  
GTTGACCGCGTCATGCGGTTGCGTGCGGGAAGCACCGCGAAAGACCTGACGTGCGATCAGGCAGAGAGCGCGCGGCG  
ACCCCTTGCGGCGCCGACC

Sequence origin: TIGR;

**FIG. 2Q**

***Staphylococcus aureus* NCTC 8325 (117 aa)**

Amino acid sequence:

MLLEKAYRIKKNADFQRIYKKGHSVANRQFVVYTCNNKEIDHFRLGISVSKKLGNVLRNLIKRAIRENFKVHKSHI  
LAKDIIIVARQPAKDMTTLQIQNSLEHVLKIAKVFNKKIK

Nucleotide sequence (plus strand):

GTTATAAGCTCAATAGAAGTTTAAATATAGCTTCAAATAAAAAACGATAAATAAGCGAGTGATGTTATTGGAAAAAGC  
TTACCGAATTAAAAAGAATGCAGATTTTCAGAGAATATATAAAAAAGGTCATTCTGTAGCCAACAGACAATTTGTTG  
TATACACTTGTAATAATAAAGAAATAGACCATTTTCGCTTAGGTATTAGTGTTTCTAAAAAACTAGGTAATGCAGTG  
TTAAGAAACAAGATTAAAAAGAGCAATACGTGAAAATTTCAAAGTACATAAGTCGCATATATTGGCCAAAGATATTAT  
TGTAATAGCAAGACAGCCAGCTAAAGATATGACGACTTTACAAATACAGAATAGTCTTGAGCACGTACTTAAAATTG  
CCAAAGTTTTTAATAAAAAAGATTAAGTAAGGATAGGGTAGGGGAAGGAAAACATTAACCACTCAACACATCCCGAAG  
TCTTACCTCAGA

Sequence origin: University of Oklahoma ACGT; Contig 561

**FIG. 2R**

***Staphylococcus aureus* COL (117 aa)**

Amino acid sequence:

MLLEKAYRIKKNADFQRIYKKGHSVANRQFVVYTCNNKEIDHFRLGISVSKKLGNVLRNLIKRAIRENFKVHKSHI  
LAKDIIIVARQPAKDMTTLQIQNSLEHVLKIAKVFNKKIK

Nucleotide sequence (plus strand):

GTTATAAGCTCAATAGAAGTTTAAATATAGCTTCAAATAAAAAACGATAAATAAGCGAGTGATGTTATTGGAAAAAGC  
TTACCGAATTAAAAAGAATGCAGATTTTCAGAGAATATATAAAAAAGGTCATTCTGTAGCCAACAGACAATTTGTTG  
TATACACTTGTAATAATAAAGAAATAGACCATTTTCGCTTAGGTATTAGTGTTTCTAAAAAACTAGGTAATGCAGTG  
TTAAGAAACAAGATTAAAAAGAGCAATACGTGAAAATTTCAAAGTACATAAGTCGCATATATTGGCCAAAGATATTAT  
TGTAATAGCAAGACAGCCAGCTAAAGATATGACGACTTTACAAATACAGAATAGTCTTGAGCACGTACTTAAAATTG  
CCAAAGTTTTTAATAAAAAAGATTAAGTAAGGATAGGGTAGGGGAAGGAAAACATTAACCACTCAACACATCCCGAAG  
TCTTACCTCAGA

Sequence origin: TIGR;

**FIG. 2S**